

tctggcagac cctacaatgg tttcgcttcc catttcttcc ccaatgctcc tatctacaac 240
gaccgtgaac gcctccagat ttacatctt gatgctggta ttctagccgt ctgttatgg 300
ctttaccgtt acgctgttgc acaaggacta gcctcaatga tctgtctaaa cggagttccg 360
cttctgatag ttaactttt cctcgcttgc atcaacttact tacaacacac tcaccctgctg 420
ttgcctcaact atgattcatc agagtggtat tggcttagag gagctttgc tactgttagac 480
agagactatg gaatcttgc caaggtgttc cataacatca cagacaccca cgtcgacac 540
cact 544

a
unt
<210> 3
<211> 1855
<212> DNA
<213> *Lesquerella fendleri*

<220>
<221> gene
<222> (1)..(1855)
<223> genomic clone encoding pLesq-HYD

<400> 3
atgaagcttt ataagaagtt agtttctt ggtgacagag aaattntgtc aattggtagt 60
gacagttgaa gcaacacaggaa caacaaggat ggttggtgnt gatgctgatg tggtgatgtg 120
ttattcatca aatactaaat actacattac ttgttgcgc ctacttctcc tatttctcc 180
gccaccatt ttggacccac ganccttca tttaaaccct ctctcggtctt attcaccaga 240
agagaagcca agagagagag agagagaatg ttctgaggat cattgtctt ttcattcgta 300
ttaacgtaaag tttttttgtt ccactcatat ctaaaatcta gtacatgca tagattaatg 360
actgttctt ctttgatat tttcagctt ttgaattcaa gatgggtctt ggtggaaagaa 420
taatggttac cccctcttcc aagaaatcag aaactgaagc cctaaaacgt ggaccatgtg 480
agaaaccacc attcaactgtt aaagatctga agaaagcaat cccacagcat tgtttcaagc 540
gctctatccc tcgttcttcc tcctaccttcc tcacagatat cacttttagt tcttgcttct 600
actacgttgc cacaaattac ttctcttcc ttccctcagcc tctctctact tacctagctt 660
ggcctcttca ttgggtatgt caaggctgtg tcttaaccgg tatctgggtc attggccatg 720
aatgtgtca ccatgcattt cgtactatc aatgggtaga tgacactgtt ggttttatct 780
tccatttcctt ccttctcgcc ccttacttctt cctggaaata cagtcatcg tgcaccatt 840
ccaacaatgg atctctcgag aaagatgaag tctttgtccc accgaagaaa gctgcagtca 900
aatggatgt taaatacctt aacaaccctt ttggacgcatttcttgcatttca acagttcagt 960
ttatccttgg gtggcccttgc tatctagctt ttaatgtatc aggttagacat tatgtatggtt 1020
tcgttccaca ttttttccctt catgcaccta tctttaaaga ccgagaacgc ctccagatat 1080
acatctcaga tgctggattt ctatgttgc ttatgggtctt ttaccgttac gctgcttac 1140
aaggatttgc tgctatgtc tgctgtatg ggttgcattt gttatgggtt aacttttcc 1200
ttgtcttggta aactttttttt cagcacactt accttcgtt accttcattt gattcaacgg 1260
agtggaaatg gattagagga gctttggta cggtagacag agactatggaa atattgaaca 1320
agggtttcca taacataaca gacacacatg tggctcatca tcttttgc actataaccgc 1380
attataacgc aatggaaatg acagaggcga taaaggcaat acttgggtat tactaccact 1440
tcgtatggaaac accgtggat gttggccatgtt atagggaaagc aaaggaggatg ctctatgttag 1500
aaccggatac ggaacgtggg aagaaagggtt tctacttata caacaataag ttatggggct 1560
gataggccga gagaagtgcatttcaatttcaatc ttcatgttca tttttttttt gttttttttt 1620
agaagctatg ctttttttca ataatctcag agtccatnta gttgtgttctt ggtgcattttt 1680
gccttagttt gttgtgttgc aagtttagtgc tcaaactgcttccatgttgc tggcccaatgt 1740
aagaacaatg ttacgtgtttt aaaatactcg gaacgaattt accacaanat atccaaaacc 1800
ggctatccga attccatatac cggaaaaccgg atatccaaat ttccagagta ctttag 1855

<210> 4
<211> 384
<212> PRT
<213> *Lesquerella fendleri*

<400> 4

Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser
1 5 10 15

Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr
20 25 30

Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser
35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
65 70 75 80

Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
85 90 95

Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala
100 105 110

Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His
115 120 125

Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg
130 135 140

His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro
145 150 155 160

Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro
165 170 175

Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro
180 185 190

Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala
195 200 205

Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu
210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
225 230 235 240

Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr
245 250 255

Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe
260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp
275 280 285

Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile

a
cont

290

295

300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
305 310 315 320

Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala
325 330 335

Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp
340 345 350

Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro
355 360 365

Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu
370 375 380

<210> 5

<211> 387

<212> PRT

<213> Ricinus communis

<400> 5

Met Gly Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser
1 5 10 15

Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
20 25 30

Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
35 40 45

Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
50 55 60

Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
65 70 75 80

Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
85 90 95

Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
100 105 110

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
115 120 125

Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
130 135 140

His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
145 150 155 160

1
a
CN

Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
165 170 175

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
180 185 190

Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
195 200 205

Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
210 215 220

Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
225 230 235 240

Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
245 250 255

Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
260 265 270

Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
275 280 285

Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
290 295 300

Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
305 310 315 320

Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
325 330 335

Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
340 345 350

Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
355 360 365

Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
370 375 380

Asn Lys Tyr
385

*A
CON*

<210> 6
<211> 383
<212> PRT
<213> Arabidopsis thaliana

<400> 6
Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
1 5 10 15

Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
20 25 30

Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
65 70 75 80

Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
85 90 95

Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145 150 155 160

Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
165 170 175

Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
195 200 205

His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
210 215 220

Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
225 230 235 240

Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
245 250 255

Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
260 265 270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
275 280 285

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
290 295 300

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
305 310 315 320

Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
325 330 335

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Cont*

Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr
340 345 350

Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
355 360 365

Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
370 375 380

<210> 7
<211> 384
<212> PRT
<213> Brassica napus

<220>
<221> PEPTIDE
<222> (1)..(384)
<223> encodes for hydroxylane enzyme for Brassica napus

<400> 7
Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
1 5 10 15

Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
35 40 45

Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro
65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe
100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg
145 150 155 160

Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Thr Phe Gly
165 170 175

Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr
180 185 190

A
CMT

Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys
195 200 205

His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
210 215 220

Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu
225 230 235 240

Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg
245 250 255

Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu
260 265 270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
275 280 285

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
290 295 300

Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu
305 310 315 320

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
325 330 335

Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val
340 345 350

Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
355 360 365

Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu Xaa
370 375 380

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cont.

<210> 8
<211> 309
<212> PRT
<213> Glycine max

<400> 8
Ser Leu Leu Thr Ser Phe Ser Tyr Val Val Tyr Asp Leu Ser Phe Ala
1 5 10 15

Phe Ile Phe Tyr Ile Ala Thr Thr Tyr Phe His Leu Leu Pro Gln Pro
20 25 30

Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu
35 40 45

Leu Thr Arg Val Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val

50	55	60
Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val Pro Tyr		
65	70	75
Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr Gly Ser		
85	90	95
Leu Asp Arg Asp Glu Arg Val Lys Val Ala Trp Phe Ser Lys Tyr Leu		
100	105	110
Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile		
115	120	125
Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp		
130	135	140
Ser Phe Ala Ser His Tyr His Pro Tyr Arg Val Arg Leu Leu Ile Tyr		
145	150	155
Val Ser Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val		
165	170	175
Ala Thr Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro		
180	185	190
Leu Leu Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Arg Val		
195	200	205
His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr		
210	215	220
Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr		
225	230	235
Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His		
245	250	255
Leu Arg Val Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp Thr		
260	265	270
Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr Val		
275	280	285
Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg Asn		
290	295	300
Lys Tyr Leu Arg Val		
305		

<210> 9
 <211> 302
 <212> PRT
 <213> Glycine max

<400> 9

Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe Cys Leu Tyr Tyr
1 5 10 15

Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro Leu Ser Phe Arg
20 25 30

Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile Leu Thr Gly Val
35 40 45

Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly
50 55 60

Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr
65 70 75 80

Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu
85 90 95

Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg
100 105 110

Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu
115 120 125

Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr
130 135 140

Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu
145 150 155 160

Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala
165 170 175

Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe
180 185 190

Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp
195 200 205

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
210 215 220

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
225 230 235 240

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Val Glu Tyr
245 250 255

Tyr Arg Phe Asp Glu Thr Pro Phe Val Lys Ala Met Trp Arg Glu Ala
260 265 270

Arg Glu Cys Ile Tyr Val Glu Pro Asp Gln Ser Thr Glu Ser Lys Gly
275 280 285

Val Phe Trp Tyr Asn Asn Lys Leu Ala Met Glu Ala Thr Val
290 295 300

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a
cont.

<210> 10
<211> 372
<212> PRT
<213> Zea mays

<220>
<221> PEPTIDE
<222> (372)
<223> Desaturase

<400> 10
Met Gly Ala Gly Gly Arg Met Thr Glu Lys Glu Arg Glu Lys Gln Glu
1 5 10 15
Gln Leu Ala Arg Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val
20 25 30
Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro
35 40 45
His Cys Phe Glu Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His
50 55 60
Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile
65 70 75 80
Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp
85 90 95
Ile Ala Gln Gly Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val
100 105 110
Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys
115 120 125
Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp
130 135 140
Glu Val Phe Val Pro Lys Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro
145 150 155 160
Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln
165 170 175
Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser Gly Arg
180 185 190
Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr
195 200 205
Asn Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala Gly Val Val
210 215 220
Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp
225 230 235 240

A
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cont.

Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp
245 250 255

Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His
260 265 270

Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met
275 280 285

Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp
290 295 300

Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
305 310 315 320

Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His
325 330 335

Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu
340 345 350

Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn
355 360 365

Lys Lys Phe Xaa
370

<210> 11

<211> 224

<212> PRT

<213> Ricinus communis

A
cont
<400> 11

Trp Val Met Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln
1 5 10 15

Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys Leu Leu Val
20 25 30

Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr
35 40 45

Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser
50 55 60

Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met
65 70 75 80

Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe
85 90 95

Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro
100 105 110

Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser
115 120 125

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile
130 135 140

Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu
145 150 155 160

Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His
165 170 175

Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly
180 185 190

Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe
195 200 205

His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro
210 215 220

<210> 12

<211> 20

<212> DNA

<213> Ricinus communis

<400> 12

gctctttgt gcgcgttac

20

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: homologous
regions of Ricinus communis deduced by hydroxylase
sequence and Arabidopsis thaliana deduced desaturase
sequence for use as oligonucleotide primer

<400> 13

cggttaccaga aaacgccttg

20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<222> (1)..(20)

<223> n is any nucleotide in mixed oligonucleotide
primer

l
a
cont

<220>
<223> Description of Artificial Sequence: homologous
regions of Ricinus communis deduced by hydroxylase
sequence and Arabidopsis thaliana deduced
desaturase sequence for u

<400> 14
taywsncaym gnmgnccayca

20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: homologous
regions of Ricinus communis deduced by hydroxylase
sequence and Arabidopsis thaliana deduced
desaturase sequence for u

1 a
cont
<220>
<221> primer_bind
<222> (1)..(21)
<223> n is any nucleotide in mixed oligonucleotide
primer

<400> 15
rtgrtgngcn acrtgngtrt c

21